

CLAIMS

1. Method of genetic modification of a TGB-3 wild type viral sequence for reducing or suppressing the possible deleterious effects of the agronomic properties of a transformed plant or plant cell by said TGB-3 viral sequence, comprising the following successive steps :
- submitting said sequence to point mutation(s) which allow the substitution of at least one amino-acid into a different amino-acid,
 - 10 - selecting genetically modified TGB-3 wild type viral sequences having said point mutation(s) and which are not able to promote cell-to-cell movement of a mutant virus having a dysfunctional TGB-3 wild type viral sequence, when expressed in trans from a replicon,
 - 15 - further selecting among said genetically modified TGB-3 viral sequences, the specifically genetically modified sequence which inhibits infection with a co-inoculated wild type virus when the mutant form was expressed from a replicon, and
 - 20 - recovering said specifically genetically modified TGB-3 viral sequence.

2. Method according to claim 1, wherein the TGB-3 wild type viral sequence is the BNYVV P15 sequence.

3. Genetically modified TGB-3 viral sequence
25 obtained by the method according to claim 1 or 2.

4. Genetically modified TGB-3 viral sequence according to claim 3, being selected from the group consisting of the following sequences :

SEQ ID NO 1 :

- 30 ATGGTGCTTGTGGTTTCAGTAGCTTTATCTAATATTGTATTGTACATAGTTGCCGGTTGT 60
M V L V V A V A L S N I V L Y I V A G C

GTTGTTGTCAGTATGTTGTA CTACCGTTTTTCAGCAACGATGTTAAAGCGTCCAGCTAT 120
V V V S M L Y S P F F S N D V K A S S Y

GCGGGAGCAATTTTAAAGGGGAGCGGCTGTATCATGGACAGGAATTCGTTTGCTCAATTT 180
5 A G A I F K G S G C I M D R N S F A Q F

GGGAGTTGCGATATTCCAAAGCATGTAGCCGAGTCCATCACTAAGGTTGCCACCAAAGAG 240
G S C D I P K H V A E S I T K V A T K E

10 CACGATGTTGACATAATGGTAAAAAGGGGTGAAGTGACCGTTCGTGTTGTGACTCTCACC 300
H D V D I M V K R G E V T V R V V T L T

GAAACTATTTTTATAATATTATCTAGATTGTTTGGTTTGGCGGTGTTTTGTTCATGATA 360
E T I F I I L S R L F G L A V F L F M I

15 TGTTTAATGTCTATAGTTTGGTTTGGTATCATAGATAA 399
C L M S I V W F W Y H R *

SEQ ID NO 2 :

20 ATGGTGCTTGTGGTTAAAGTAGATTTATCTAATATTGTATTGTACATAGTTGCCGGTTGT 60
M V L V V K V D L S N I V L Y I V A G C

GTTGTTGTCAGTATGTTGTA CTACCGTTTTTCAGCAACGATGTTAAAGCGTCCAGCTAT 120
V V V S M L Y S P F F S N D V K A S S Y

25 GCGGGAGCAATTTTAAAGGGGAGCGGCTGTATCATGGCCCGAATTCGTTTGCTCAATTT 180
A G A I F K G S G C I M A A N S F A Q F

GGGAGTTGCGATATTCCAAAGCATGTAGCCGAGTCCATCACTAAGGTTGCCACCAAAGAG 240
30 G S C D I P K H V A E S I T K V A T K E

CACGATGTTGACATAATGGTAAAAAGGGGTGAAGTGACCGTTCGTGTTGTGACTCTCACC 300
H D V D I M V K R G E V T V R V V T L T

GAAACTATTTTTATAATATTATCTAGATTGTTTGGTTTGGCGGTGTTTTGTTCATGATA 360
E T I F I I L S R L F G L A V F L F M I

TGTTTAATGTCTATAGTTTGGTTTTGGTATCATAGATAA 399

5 C L M S I V W F W Y H R *

SEQ ID NO 3 :

ATGGTGCTTGTGGTTAAAGTAGATTTATCTAATATTGTATTGTACATAGTTGCCGGTGT 60
M V L V V K V D L S N I V L Y I V A G C

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GTTGTTGTCAGTATGTTGTACTCACCGTTTTTCAGCAACGATGTTAAAGCGTCCAGCTAT 120
V V V S M L Y S P F F S N D V K A S S Y

GCGGGAGCAATTTTTAAGGGGAGCGGCTGTATCATGGACAGGAATTCGTTTGCTCAATTT 180

15 A G A I F K G S G C I M D R N S F A Q F

GGGAGTTGCGATATTCCAAAGCATGTAGCCGAGTCCATCACTAAGGTTGCCACCAAAGAG 240
G S C D I P K H V A E S I T K V A T K E

20 CACGATGTTGACATAATGGTAAAAAGGGGTGAAGTGACCGTTCGTGTTGTGACTCTCACC 300
H D V D I M V K R G E V T V R V V T L T

GAACTATTTTTATAATATTATCTAGATTGTTTGGTTTGGATGATTTTTGTTCATGATA 360
E T I F I I L S R L F G L D D F L F M I

25

TGTTTAATGTCTATAGTTTGGTTTTGGTATCATAGATAA 399

C L M S I V W F W Y H R *

5. Vector comprising the genetically modified
30 TGB-3 viral sequence according to the claim 3 or 4,
possibly linked to one or more regulatory sequence(s)
capable of being active into a plant or a plant cell.

6. Method for inducing resistance into a plant or a plant cell to a virus comprising a TGB-3 sequence, comprising the following steps :

- preparing a nucleic acid construct comprising a
5 genetically modified TGB-3 viral sequence according to claim 4 or 5, being operably linked to one or more regulatory sequence(s) capable of being active into a plant or a plant cell,
- transforming a plant cell with said nucleic acid
10 construct, and possibly
- regenerating a transgenic plant from the transformed plant cell.

7. Method according to claim 6, characterised in that the virus is selected from the group consisting of
15 the apple stem pitting virus, the blueberry scorch virus, the potato virus M, the white clover mosaic virus, the *Cymbidium* mosaic virus, the barley stripe mosaic virus, the potato mop top virus, the peanut clump virus, the beet soil-borne virus or the BNYVV virus.

20 8. Method according to claim 6 or 7, characterised in that the plant cell is a stomatal cell.

9. Method according to any one of the claims 6 to 8, characterised in that the plant is selected from the group consisting of apple, blueberry, potato, clover,
25 orchid, barley, peanut or sugar beet.

10. Method according to any one of the claims 6 to 9, characterised in that the regulatory sequence comprises a promoter sequence or a terminator sequence active in a plant.

30 11. Method according to claim 10, characterised in that the promoter sequence is a constitutive or a foreigner promoter sequence.

12. Method according to claim 10, characterised in that the promoter sequence is selected from the group consisting of 35S Cauliflower Mosaic Virus promoter, and/or the polyubiquitin *Arabidopsis thaliana* promoter.

13. Method according to any one of the claims 10 to 12, characterised in that the promoter sequence is a promoter which is capable of being active mainly into the root tissue of plants such as the par promoter of the haemoglobin gene from *Perosponia andersonii*.

14. Transgenic plant or transgenic plant cell resistant to a virus and comprising a nucleic acid construct having a genetically modified TGB-3 viral sequence according to claim 4 or 5, being operably linked to one or more regulatory sequence(s) active into a plant or a plant cell.

15. Transgenic plant or transgenic plant cell according to claim 14, characterised in that the virus is selected from the group consisting of the apple stem pitting virus, the blueberry scorch virus, the potato virus M, the white clover mosaic virus, the *Cymbidium* mosaic virus, the potato virus X, the barley stripe mosaic virus, the potato mop top virus, the peanut clump virus, the beet soil-borne virus and the BNYVV virus.

16. Transgenic plant or transgenic plant cell according to claim 14 or 15, being a plant or a plant cell selected from the group consisting of apple, blueberry, potato, clover, orchid, barley, peanut or sugar beet plant or plant cell.

17. Transgenic plant or transgenic plant cell according to any one of the claims 14 to 16, characterised in that the regulatory sequence comprises a promoter

sequence and a terminator sequence capable of being active into a plant.

18. Transgenic plant or transgenic plant cell according to any one of the claims 14 to 17, characterised
5 in that the regulatory sequence(s) comprise a promoter sequence which is a constitutive or a foreigner vegetal promoter sequence.

19. Transgenic plant or transgenic plant cell according to claim 18, characterised in that promoter
10 sequence is selected from the group consisting of 35S Cauliflower Mosaic Virus promoter, and/or the polyubiquitin Arabidopsis thaliana promoter.

20. Transgenic plant or transgenic plant cell according to claim 18 or 19, characterised in that the
15 promoter sequence is a promoter which is mainly active in root tissues such as the par promoter of the haemoglobin gene from *Perosponia andersonii*.

21. Transgenic plant tissue selected from the group consisting of fruit, stem, root, tuber, seed of a
20 plant according to any one of the claims 14 to 20.

22. Reproducible structure obtained from a transgenic plant according to any one of the claims 14 to 21.